

A: 40  
 X1: 16 ( 7.4 bits)  
 X2: 38 (14.8 bits)  
 X3: 64 (24.9 bits)  
 S1: 41 (21.9 bits)  
 S2: 63 (29.0 bits)  
 BLASTP 2.0.9 [May-07-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 47-14-1-C3-CL0\_5C  
 (351 letters)

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens  
 113,759 sequences; 24,820,038 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
GSP:Y35918 Y35918 Extended human secreted protein sequence, SEQ...	735	0.0
STR:Q9ULS1 Q9ULS1 KIAA1149 PROTEIN (FRAGMENT). >GNP:AB032975 AB...	684	0.0
GSP:Y88438 Y88438 Modified human aspartyl protease 2 (Asp2) ami...	655	0.0
GNP:AF200193 AF200193_1 Homo sapiens memapsin 2 mRNA, partial c...	655	0.0
SP:P56817 Q9UJT5 BACE_HUMAN BETA-SECRETASE PRECURSOR (EC 3.4.23...	655	0.0
GSP:Y88439 Y88439 Modified human aspartyl protease 2 (Asp2) ami...	655	0.0
GSP:Y88437 Y88437 Human Asp2 amino acid sequence containing pro...	653	0.0
GSP:Y88425 Y88425 Human aspartyl protease 2 (a) (Asp2) amino ac...	653	0.0
GSP:Y88431 Y88431 T7-caspase-human-pro-Asp-2(a)-deltaTM amino a...	653	0.0
GSP:Y88432 Y88432 T7-caspase-human-pro-Asp-2(a)-deltaTM amino a...	653	0.0
GSP:Y88433 Y88433 Human-pro-Asp-2(a)-deltaTM amino acid sequence.	653	0.0
GSP:W59807 W59807 Amino acid sequence of human ASP2 (aspartic p...	653	0.0
GSP:W59808 W59808 Partial amino acid sequence of human ASP2 (as...	649	0.0
GSP:Y88426 Y88426 Human aspartyl protease 2 (b) (Asp2) amino ac...	592	e-169
GNP:AF200192 AF200192_1 Homo sapiens memapsin 1 mRNA, complete ...	362	e-100
SP:Q9Y5Z0 Q9UJT6 BAE2_HUMAN BETA SECRETASE 2 PRECURSOR (EC 3.4....	362	e-100
STR:CAB90554 CAB90554 Beta-site APP-cleaving enzyme 2, EC 3.4.2...	362	e-100
STR:AAF28927 AAF28927 HSPC104 (Fragment). >GNP:AF161367 AF16136...	300	3e-81
STR:AAF35836 AAF35836 Aspartyl protease. >GNP:AF188277 AF188277...	299	4e-81
STR:AAF35835 AAF35835 Aspartyl protease. >GNP:AF188276 AF188276...	262	5e-70
GSP:Y11427 Y11427 Human 5' EST secreted protein SEQ ID No 249.	118	2e-26
SP:P00790 PEPA_HUMAN PEPSIN A PRECURSOR (EC 3.4.23.1). >PIR:A00...	81	2e-15
PIR:A30142 S02664 S02542 PX0027 PX0025 PX0026 A22434 A30142 pep...	80	7e-15
GNP:M26032 M26032_1 Human pepsinogen A (15.0) gene, exon 9, clo...	80	7e-15
PIR:B30142 E22434 B30142 pepsin A (EC 3.4.23.1) 4 precursor - h...	79	1e-14
SP:P14091 CATE_HUMAN CATHEPSIN E PRECURSOR (EC 3.4.23.34). >PIR...	78	1e-14
SP:P07339 CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5). >GSP:...	76	1e-13
SP:P20142 PEPC_HUMAN GASTRICIN PRECURSOR (EC 3.4.23.3) (PEPSIN...	71	2e-12
GNP:M18667 M18667_1 Human pepsinogen C gene, exon 9, clone cosH...	71	2e-12
GSP:Y31744 Y31744 Human protease HPRM-3.	63	7e-10
STR:CAB82849 CAB82849 Cathepsin E, alternative precursor (EC 3....	63	7e-10
SP:P00797 RENI_HUMAN RENIN PRECURSOR, RENAL (EC 3.4.23.15) (ANG...	55	1e-07
GSP:P50135 P50135 Sequence of pre-pro-renin.	55	1e-07
GSP:W23244 W23244 Human renin.	55	1e-07
STR:Q15296 Q15296 KIDNEY MRNA FRAGMENT FOR RENIN (AA 105-401) (...	55	2e-07
GNP:M26901 M26901_1 Human renin gene, exon 9; precursor.	52	1e-06
GSP:W54877 W54877 Human napsin A protein.	38	0.030
GSP:W57042 W57042 Human aspartic protease SEQ ID NO:1.	38	0.030
GSP:Y44810 Y44810 Human Aspartic Protease-2 (NHAP-2).	38	0.030
STR:Q9UHB3 Q9UHB3 ASPARTYL PROTEASE 3 (FRAGMENT). >GNP:AF200344...	38	0.030
SP:O96009 NAP1_HUMAN NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A...	37	0.052
GSP:W37958 W37958 Amino acid sequence of human cathepsin polype...	37	0.052
GSP:Y06435 Y06435 Human protease HUPM-4. >GSP:Y44809 Y44809 Hum...	37	0.052
GSP:W57043 W57043 Human aspartic protease encoding cDNA SEQ ID ...	36	0.088
PIR:T08737 T08737 hypothetical protein DKFZp566O1646.1 - human ...	34	0.45
STR:AAF86877 AAF86877 DC8. >GNP:AF201941 AF201941_1 Homo sapien...	34	0.45
RTR:AAD53859 AAD53859 IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGIO...	32	1.7
SP:Q99712 Q99446 O00564 IRKF_HUMAN ATP-SENSITIVE INWARD RECTIFI...	29	8.7
GNP:D87291 D87291_1 Human mRNA for inward rectifier potassium c...	29	8.7
GNP:Y10745 Y10745_1 H.sapiens mRNA for inwardly rectifying potas...	29	8.7

>GSP:Y35918|Y35918|Extended human secreted protein sequence, SEQ ID

NO. 167.  
Length = 351

Score = 735 bits (1878), Expect = 0.0  
Identities = 351/351 (100%), Positives = 351/351 (100%)

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Query: 1  MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI 60
      MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI
Sbjct: 1  MVPFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANI 60

Query: 61  AAITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF 120
      AAITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF
Sbjct: 61  AAITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGF 120

Query: 121  PLNQSEVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKE 180
      PLNQSEVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKE
Sbjct: 121  PLNQSEVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKE 180

Query: 181  YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI 240
      YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI
Sbjct: 181  YNYDKSIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI 240

Query: 241  FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 300
      FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
Sbjct: 241  FPVISLYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 300

Query: 301  GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351
      GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR
Sbjct: 301  GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351
```

>STR:Q9ULS1|Q9ULS1|KIAA1149 PROTEIN (FRAGMENT).  
>GNP:AB032975|AB032975\_1|Homo sapiens mRNA for KIAA1149  
protein, partial cds; Start codon is not identified..  
Length = 396

Score = 684 bits (1745), Expect = 0.0  
Identities = 330/333 (99%), Positives = 330/333 (99%)

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Query: 6  YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE 65
      YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE
Sbjct: 1  YLQAHFTLCSGWSSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITE 60

Query: 66  SDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS 125
      SDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS
Sbjct: 61  SDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQS 120

Query: 126  EVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 185
      EVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK
Sbjct: 121  EVLASVGGSMIIGGIDHSlyTGS LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDK 180

Query: 186  SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS 245
      SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS
Sbjct: 181  SIVDSGTTNLR LPKKVFEAAVKS IKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVIS 240

Query: 246  LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 305
      LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV
Sbjct: 241  LYLMGEVTNQSFRTILPQQYL RPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYV 300

Query: 306  FDRARKRIGFAVSACHVHDEFRTAAVEGPFCHL 338
      FDRARKRIGFAVSACHVHDEFRTAAVEGPF L
Sbjct: 301  FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTL 333
```

>GSP:Y88438|Y88438|Modified human aspartyl protease 2 (Asp2) amino  
acid sequence.  
Length = 453

Score = 655 bits (1672), Expect = 0.0  
Identities = 318/321 (99%), Positives = 318/321 (99%)

```
Query: 18  SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77
      SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE
Sbjct: 118  SSTYRDLRKGVVYPYTQGKWEDELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78  GILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMI 137
      GILGLAYAEIARPDDSPPEFFDSL VKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMI
```

Sbjct: 178 GILGLAYAEIARPDSDLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 238 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 357

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417

Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
SACHVHDEFRTAAVEGPF L

Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GNP:AF200193|AF200193\_1|Homo sapiens memapsin 2 mRNA, partial cds;  
membrane-associated aspartic protease 2.  
Length = 488

Score = 655 bits (1672), Expect = 0.0  
Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77  
SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 105 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 164

Query: 78 GILGLAYAEIARPDSDLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
GILGLAYAEIARPDSDLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII

Sbjct: 165 GILGLAYAEIARPDSDLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 224

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 225 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 284

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF

Sbjct: 285 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 344

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 345 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 404

Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
SACHVHDEFRTAAVEGPF L

Sbjct: 405 SACHVHDEFRTAAVEGPFVTL 425

>SP:P56817 Q9UJT5|BACE\_HUMAN|BETA-SECRETASE PRECURSOR (EC 3.4.23.-)  
(BETA-SITE APP CLEAVING ENZYME) (BETA-SITE AMYLOID  
PRECURSOR PROTEIN CLEAVING ENZYME) (ASPARTYLPROTEASE 2)  
(ASP 2) (ASP2) (MEMBRANE-ASSOCIATED ASPARTIC PROTEASE  
2) (MEMAPSIN-2). >PIR:A59090|A59090|aspartic proteinase  
(EC 3.4.23.-) BACE precursor - human  
>STR:AAF26367|AAF26367|Transmembrane aspartic proteinase  
Asp 2. >GNP:AF190725|AF190725\_1|Homo sapiens beta-site  
APP cleaving enzyme (BACE) mRNA, complete cds.  
>GNP:AF200343|AF200343\_1|Homo sapiens chromosome 11  
aspartyl protease 2 mRNA, complete cds.  
>GNP:AF201468|AF201468\_1|Homo sapiens APP beta-secretase  
mRNA, complete cds; membrane type aspartyl protease.  
>GNP:AF204943|AF204943\_1|Homo sapiens transmembrane  
aspartic proteinase Asp 2 (BACE1) mRNA, complete cds;  
beta-site APP processing enzyme.  
Length = 501

Score = 655 bits (1672), Expect = 0.0  
Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 77  
SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 118 SSTYRDLRKGIVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDSDLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137

Sbjct: 178 GILGLAYAEIARPDDES EPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 237  
 Query: 138 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 238 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297  
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF  
 Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 357  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417  
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88439|Y88439|Modified human aspartyl protease 2 (Asp2) amino  
 acid sequence.  
 Length = 459

Score = 655 bits (1672), Expect = 0.0  
 Identities = 318/321 (99%), Positives = 318/321 (99%)

Query: 18 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 118 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177  
 Query: 78 GILGLAYAEIARPDDESPEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDDES EPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 178 GILGLAYAEIARPDDESLEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 237  
 Query: 138 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 238 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297  
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF  
 Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 357  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417  
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88437|Y88437|Human Asp2 amino acid sequence containing  
 proteolytic cleavage site.  
 Length = 425

Score = 653 bits (1667), Expect = 0.0  
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 90 SSTYRDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 149  
 Query: 78 GILGLAYAEIARPDDESPEPFFDSLQKTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDDES EPFFDSLQKTHVPNLFSL LCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 150 GILGLAYAEIARPDDESLEPFFDSLQKTHVPNLFSLHLCGAGFPLNQSEVLASVGGSMII 209  
 Query: 138 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 210 GGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 269  
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF  
 Sbjct: 270 PKKVFEAAVKSIIKAASSTEKFPDGFQWLGELQVCWQAGTTPWNIFPVISLYLMGEVTNQSF 329  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 330 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 389

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 390 SACHVHDEFRTAAVEGPFVTL 410

>GSP:Y88425|Y88425|Human aspartyl protease 2 (a) (Asp2) amino acid sequence.

Length = 501

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77

SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 118 SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137

GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLCGAGFPLNQSEVLASVGGSMII

Sbjct: 178 GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLHLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197

GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 238 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257

PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 357

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317

RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:Y88431|Y88431|T7-caspase-human-pro-Asp-2(a)-deltaTM amino acid sequence.

Length = 446

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77

SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE

Sbjct: 111 SSTYRDLRKGVVVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 170

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLCGAGFPLNQSEVLASVGGSMII 137

GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLCGAGFPLNQSEVLASVGGSMII

Sbjct: 171 GILGLAYAEIARPDSPPEFFDSLQKQTHVNLFSLLHLCGAGFPLNQSEVLASVGGSMII 230

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197

GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL

Sbjct: 231 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 290

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257

PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF

Sbjct: 291 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 350

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317

RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV

Sbjct: 351 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 410

Query: 318 SACHVHDEFRTAAVEGPFCHL 338

SACHVHDEFRTAAVEGPF L

Sbjct: 411 SACHVHDEFRTAAVEGPFVTL 431

>GSP:Y88432|Y88432|T7-caspase-human-pro-Asp-2(a)-deltaTM amino acid sequence.

Length = 459

Score = 653 bits (1667), Expect = 0.0

Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 124 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 183

Query: 78 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSL LCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 184 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLHLCGAGFPLNQSEVLASVGGSMII 243

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 244 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 303

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF  
 Sbjct: 304 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 363

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 364 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 423

Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 424 SACHVHDEFRTAAVEGPFVTL 444

>GSP:Y88433|Y88433|Human-pro-Asp-2(a)-deltaTM amino acid sequence.  
 Length = 433

Score = 653 bits (1667), Expect = 0.0  
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 98 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 157

Query: 78 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSL LCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 158 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLHLCGAGFPLNQSEVLASVGGSMII 217

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 218 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 277

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF  
 Sbjct: 278 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 337

Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 338 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 397

Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 398 SACHVHDEFRTAAVEGPFVTL 418

>GSP:W59807|W59807|Amino acid sequence of human ASP2 (aspartic  
 protease 2).  
 Length = 501

Score = 653 bits (1666), Expect = 0.0  
 Identities = 317/321 (98%), Positives = 317/321 (98%)

Query: 18 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 118 SSTRYDLRKGYYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177

Query: 78 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLQLCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSL LCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 178 GILGLAYAEIARPDDSPPEFFDLSVKQTHVFNLFSLHLCGAGFPLNQSEVLASVGGSMII 237

Query: 138 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 238 GGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 297

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257

Sbjct: 298 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 357  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 358 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 417  
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 418 SACHVHDEFRTAAVEGPFVTL 438

>GSP:W59808|W59808|Partial amino acid sequence of human ASP2  
 (aspartic protease 2).  
 Length = 790

Score = 649 bits (1655), Expect = 0.0  
 Identities = 315/321 (98%), Positives = 315/321 (98%)

Query: 18 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 61 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 120  
 Query: 78 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 121 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 180  
 Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 181 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 240  
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAAS EKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF  
 Sbjct: 241 PKKVFEAAVKSIIKAASPREKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 300  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 301 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 360  
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 361 SACHVHDEFRTAAVEGPFVTL 381

>GSP:Y88426|Y88426|Human aspartyl protease 2 (b) (Asp2) amino acid  
 sequence.  
 Length = 476

Score = 592 bits (1511), Expect = e-169  
 Identities = 294/321 (91%), Positives = 294/321 (91%), Gaps = 25/321 (7%)

Query: 18 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 77  
 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE  
 Sbjct: 118 SSTYRDLRKGVPYPTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDKFFINGSNWE 177  
 Query: 78 GILGLAYAEIARPDSDPEPFFDSLQKQTHVFNLSLQCGAGFPLNQSEVLASVGGSMII 137  
 GILGLAYAEIAR LCGAGFPLNQSEVLASVGGSMII  
 Sbjct: 178 GILGLAYAEIAR-----LCGAGFPLNQSEVLASVGGSMII 212  
 Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 197  
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL  
 Sbjct: 213 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRL 272  
 Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF  
 Sbjct: 273 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFFVISLYLMGEVTNQSF 332  
 Query: 258 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 317  
 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV  
 Sbjct: 333 RITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAV 392  
 Query: 318 SACHVHDEFRTAAVEGPFCHL 338  
 SACHVHDEFRTAAVEGPF L  
 Sbjct: 393 SACHVHDEFRTAAVEGPFVTL 413

>GNP:AF200192|AF200192\_1|Homo sapiens memapsin 1 mRNA, complete cds;

membrane-associated aspartic protease 1.  
Length = 518

Score = 362 bits (919), Expect = e-100

Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRGVYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAA 62  
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA  
Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFDTVYKYTQGSWTGFVGEDLV TIPKGNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122  
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+  
Sbjct: 180 IFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSYLTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182  
S + GGS+++GGI+ SLY G +WYTP I+ EWYY++ I+++EI GQ L +DC+EYN  
Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 242  
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFW G QL CW TPW+ FP  
Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTITLPQQYL R PVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302  
IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF  
Sbjct: 357 KISIIYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 415

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335  
YV+FDRA+KR+GFA S C + + GPF  
Sbjct: 416 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 448

>SP:Q9Y5Z0 Q9UJT6|BAE2\_HUMAN|BETA SECRETASE 2 PRECURSOR (EC 3.4.23.-) (BETA-SITE APP-CLEAVING ENZYME 2) (ASPARTYL PROTEASE 1) (ASP1) (ASP1) (MEMBRANE-ASSOCIATED ASPARTIC PROTEASE 1) (MEMAPSIN-1). >GSP:W61362|W61362|Aspartic proteinase ASP1. >GSP:Y41714|Y41714|Human PRO852 protein sequence. >GSP:Y22239|Y22239|Human CSP56, aspartyl-type protease, protein sequence. >GSP:Y13799|Y13799|Human aspartyl protease, CSP56. >GSP:Y88424|Y88424|Human aspartyl protease 1 (Asp1) amino acid sequence. >GNP:AF050171|AF050171\_1|Homo sapiens aspartyl protease mRNA, complete cds. >GNP:AF117892|AF117892\_1|Homo sapiens aspartic-like protease mRNA, complete cds. >GNP:AF178532|AF178532\_1|Homo sapiens aspartyl protease (BACE2) mRNA, complete cds. >GNP:AF200342|AF200342\_1|Homo sapiens chromosome 21 aspartyl protease 1 mRNA, complete cds. >GNP:AF204944|AF204944\_1|Homo sapiens transmembrane aspartic proteinase Asp 1 (BACE2) mRNA, complete cds; beta-site APP processing enzyme. >GNP:AF178532|AF178532\_1|Homo sapiens aspartyl protease (BACE2) mRNA, complete cds.  
Length = 518

Score = 362 bits (919), Expect = e-100

Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRGVYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAA 62  
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA  
Sbjct: 122 PHSYIDTYFD--TERSSTYRSKGFDTVYKYTQGSWTGFVGEDLV TIPKGNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122  
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+  
Sbjct: 180 IFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSYLTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYN 182  
S + GGS+++GGI+ SLY G +WYTP I+ EWYY++ I+++EI GQ L +DC+EYN  
Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 242  
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFW G QL CW TPW+ FP  
Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTITLPQQYL R PVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302  
IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF  
Sbjct: 357 KISIIYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 415



Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335  
 YV+FDRA+KR+GFA S C + + GPF  
 Sbjct: 416 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 448

>STR:CAB90554|CAB90554|Beta-site APP-cleaving enzyme 2, EC 3.4.23  
 (Fragment). >GNP:AL163285|AL163285\_1|Homo sapiens  
 chromosome 21 segment HS21C085; Accession No. AF050171.  
 Length = 415

Score = 362 bits (919), Expect = e-100  
 Identities = 174/333 (52%), Positives = 230/333 (68%), Gaps = 6/333 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGNVTVRANIAA 62  
 P Y+ +F + SSTYR V V YTOG W G +G DLV+IP G N + NIA  
 Sbjct: 19 PHSYIDTYFD--TERSSSTYRSKGFVDVTVKYTGQSWTGFVGEDLVITPKGFNTSFLVNIAT 76

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVNLFSLQLCGAGFPL 122  
 I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+  
 Sbjct: 77 IFESENFFLPGIKWNGILGLAYATLAKPSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 136

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYN 182  
 S + GGS+++GGI+ SLY G +WYTP+ EWYY++ I+++EI GQ L +DC+EYN  
 Sbjct: 137 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKBEWYQIEILKLEIGGQSLNLDCKEYN 193

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242  
 DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFV G QL CW TPW+ FP  
 Sbjct: 194 ADKAIVDSGTTLLRPLQKVFDAVVEAVARSLIPEFSDGFWTGSQACWTNSETPWSYFP 253

Query: 243 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSDQDDCYKFAISQSSTGTVMGAVIMEGF 302  
 IS+YL E +++SFRITILPQ Y++P+ + +CY+F IS S+ V+GA +MEGF  
 Sbjct: 254 KISYLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGF 312

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335  
 YV+FDRA+KR+GFA S C + + GPF  
 Sbjct: 313 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 345

>STR:AAF28927|AAF28927|HSPC104 (Fragment).  
 >GNP:AF161367|AF161367\_1|Homo sapiens HSPC104 mRNA,  
 partial cds.  
 Length = 213

Score = 300 bits (759), Expect = 3e-81  
 Identities = 154/217 (70%), Positives = 164/217 (74%), Gaps = 7/217 (3%)

Query: 138 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNNDKSIVDSGTTNLR 197  
 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNNDKSIVDSGTTNLR  
 Sbjct: 1 GGIDHSLYTGSLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNNDKSIVDSGTTNLR 60

Query: 198 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 257  
 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF  
 Sbjct: 61 PKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSF 120

Query: 258 RITILPQQYLRPVE---DVATSDQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314  
 RITILPQQYLRP + T+ C+ I G+ ++ + + +  
 Sbjct: 121 RITILPQQYLRPWKMWRPRTTVTVCHLTVIHGHCYGCYHGGLPLSLIGPENELACLS 180

Query: 315 FAVSACHVHDEFRTAAVEGPFCHLGHGRLWLQHSTDR 351  
 R A+ CHLGHGRLWLQHSTDR  
 Sbjct: 181 ALAMCTMSSGRQRWKAL----CHLGHGRLWLQHSTDR 213

>STR:AAF35836|AAF35836|Aspartyl protease.  
 >GNP:AF188277|AF188277\_1|Homo sapiens aspartyl protease  
 (BACE2) mRNA, complete cds, alternatively spliced;  
 alternatively spliced; lacks exon 8.  
 >GNP:AF188277|AF188277\_1|Homo sapiens aspartyl protease  
 (BACE2) mRNA, complete cds, alternatively spliced;  
 alternatively spliced; lacks exon 8.  
 Length = 396

Score = 299 bits (758), Expect = 4e-81  
 Identities = 143/263 (54%), Positives = 186/263 (70%), Gaps = 5/263 (1%)

Query: 3 PFIYLQAHFTLCSGWSSTYRDLRKGVVYPYTGKWEGLGTDLVSIHPGNVTVRANIAA 62  
 P Y+ +F + SSTYR V V YTOG W G +G DLV+IP G N + NIA

Sbjct: 122 PHSYIDTYFD--TERSSYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122  
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+

Sbjct: 180 IFESENFFLPGLKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYN 182  
S + GGS+++GGI+ SLY G +WYTP+ EWYY++ I+++EI GQ L +DC+EYN

Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242  
DK+IVDSGTT LRLP+KVF+A V+++ AS +F DGFV G QL CW TPW+ FP

Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFP 356

Query: 243 VISLYLMGEVTNQSFRTILPQQ 265  
IS+YL E +++SFRITILPQ+

Sbjct: 357 KISYLRDENSRSFRITILPQK 379

>STR:AAF35835|AAF35835|Aspartyl protease.  
>GNP:AF188276|AF188276\_1|Homo sapiens aspartyl protease  
(BACE2) mRNA, complete cds, alternatively spliced;  
alternatively spliced; lacks exon 7.  
>GNP:AF188276|AF188276\_1|Homo sapiens aspartyl protease  
(BACE2) mRNA, complete cds, alternatively spliced;  
alternatively spliced; lacks exon 7.  
Length = 468

Score = 262 bits (663), Expect = 5e-70  
Identities = 143/333 (42%), Positives = 190/333 (56%), Gaps = 56/333 (16%)

Query: 3 PFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAA 62  
P Y+ +F + SSTYR V V YTQG W G +G DLV+IP G N + NIA

Sbjct: 122 PHSYIDTYFD--TERSSYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAT 179

Query: 63 ITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLCGAGFPL 122  
I ES+ FF+ G W GILGLAYA +A+P S E FFDSLQ Q ++PN+FS+Q+CGAG P+

Sbjct: 180 IFESENFFLPGLKWNIGLGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239

Query: 123 NQSEVLASVGGSMIIGGIDHSLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYN 182  
S + GGS+++GGI+ SLY G +WYTP+ EWYY++ I+++EI GQ L +DC+EYN

Sbjct: 240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYN 296

Query: 183 YDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 242  
DK+IVDSGTT LRLP+KVF+A V+++ AS P G C++ G +P

Sbjct: 297 ADKAIVDSGTTLLRPLQKVFDAVVEAVARASLLYIQP-MMGAGLNYECYRFGISP----- 350

Query: 243 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 302  
S+ V+GA +MEGF

Sbjct: 351 -----STNALVIGATVMEGF 365

Query: 303 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPF 335  
YV+FDRA+KR+GFA S C + + GPF

Sbjct: 366 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPF 398

>GSP:Y11427|Y11427|Human 5' EST secreted protein SEQ ID No 249.  
Length = 53

Score = 118 bits (292), Expect = 2e-26  
Identities = 52/52 (100%), Positives = 52/52 (100%)

Query: 1 MVPFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP 52  
MVPFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP

Sbjct: 1 MVPFIYLAQHFTLCSGWSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGP 52

>SP:P00790|PEPA\_HUMAN|PEPSIN A PRECURSOR (EC 3.4.23.1). >PIR:A00980  
PX0023 S02663 F22434 I54252 PX0024|PEHU|pepsin A (EC  
3.4.23.1) 3 precursor - human >GNP:J00287|J00287\_1|Human  
pepsinogen gene, exon 9; pepsinogen.  
Length = 388

Score = 81.1 bits (197), Expect = 2e-15  
Identities = 82/302 (27%), Positives = 137/302 (45%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76

```

      SSTY+   + V + Y G   G LG D V +   ++   I ++E++   F+   + +
Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77  EGILGLAYAEIARPDSPPEFFDSL VKQTHVP-NLFS LQLCGAGFPLNQSEVLASVGGSM 135
      +GILGLAY I+   P FD++ Q V +LFS+ L   +QS   G +
Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLF SVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHS LYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
      I GGID S YTGSL + P+ E Y+++ + + +NG+ +   C E   ++IVD+GT+ L
Sbjct: 228 IFGGIDSSYYTGSLNWPVPTVEGYWQITVDSITMNGEAIA--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKS IKAASSTEKFDPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
      P   I A+ +++   G+ +V C   + P +F   T
Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324

Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
      + + P Y+ E S   ++S   ++G V + ++ VFDRA ++G
Sbjct: 325 NGVQYPVPSPAYILQSEGSCISGFQGMNLP-TEGELWILGDVFIRQYFTVFD RANNQVG 383

Query: 315 FA 316
      A
Sbjct: 384 LA 385

```

>PIR:A30142 S02664 S02542 PX0027 PX0025 PX0026 A22434|A30142|pepsin  
 A (EC 3.4.23.1) 5 precursor - human  
 Length = 388

Score = 79.6 bits (193), Expect = 7e-15  
 Identities = 81/302 (26%), Positives = 137/302 (44%), Gaps = 42/302 (13%)

```

Query: 18  SSTYRDLRKG VYPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDK-FFINGSNW 76
      SSTY+   + V + Y G   G LG D V +   ++   I ++E++   F+   + +
Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77  EGILGLAYAEIARPDSPPEFFDSL VKQTHVP-NLFS LQLCGAGFPLNQSEVLASVGGSM 135
      +GILGLAY I+   P FD++ Q V +LFS+ L   +QS   G +
Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLF SVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHS LYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
      I GGID S YTGSL + P+ E Y+++ + + +NG+ +   C E   ++IVD+GT+ L
Sbjct: 228 IFGGIDSSYYTGSLNWPVPTVEGYWQITVDSITMNGEAIA--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKS IKAASSTEKFDPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
      P   I A+ +++   G+ +V C   + P +F   T
Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324

Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314
      + + P Y+ E S   ++S   ++G V + ++ VF+RA ++G
Sbjct: 325 NGVQYPVPSPAYILQSEGSCISGFQGMNLP-TEGELWILGDVFIRQYFTVFERANNQVG 383

Query: 315 FA 316
      A
Sbjct: 384 LA 385

```

>GNP:M26032|M26032\_1|Human pepsinogen A (15.0) gene, exon 9, clone  
 cgHGP2; precursor.  
 Length = 388

Score = 79.6 bits (193), Expect = 7e-15  
 Identities = 81/302 (26%), Positives = 137/302 (44%), Gaps = 42/302 (13%)

```

Query: 18  SSTYRDLRKG VYPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITESDK-FFINGSNW 76
      SSTY+   + V + Y G   G LG D V +   ++   I ++E++   F+   + +
Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG---GISDTNQIFGLSETEPGSFLYYAPF 179

Query: 77  EGILGLAYAEIARPDSPPEFFDSL VKQTHVP-NLFS LQLCGAGFPLNQSEVLASVGGSM 135
      +GILGLAY I+   P FD++ Q V +LFS+ L   +QS   G +
Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSDLF SVYLSAD----DQS-----GSVV 227

Query: 136 IIGGIDHS LYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195
      I GGID S YTGSL + P+ E Y+++ + + +NG+ +   C E   ++IVD+GT+ L
Sbjct: 228 IFGGIDSSYYTGSLNWPVPTVEGYWQITVDSITMNGEAIA--CAE--GCQAIVDTGTSLL 283

Query: 196 RLPKKVFEEAAVKS IKAASSTEKFDPDGFWLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254
      P   I A+ +++   G+ +V C   + P +F   T

```

Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324  
 Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314  
 + + P Y+ E S ++S ++G V + ++ VF+RA ++G  
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNLP-TESGELWILGDVFIRQYFTVFERANNQVG 383  
 Query: 315 FA 316  
 A  
 Sbjct: 384 LA 385

>PIR:B30142 E22434|B30142|pepsin A (EC 3.4.23.1) 4 precursor - human  
 Length = 388

Score = 78.8 bits (191), Expect = 1e-14  
 Identities = 79/302 (26%), Positives = 134/302 (44%), Gaps = 42/302 (13%)

Query: 18 SSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDK-FFINGSNW 76  
 SSTY+ + V + Y G G LG D V + ++ I ++E++ F+ + +  
 Sbjct: 123 SSTYQSTSETVSITYGTGSMTGILGYDTVQVG--GISDTNQIFGLSETEPGSFLYYAPF 179  
 Query: 77 EGILGLAYAEIARPDSPPEPFFDSLVLKQTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSM 135  
 +GILGLAY I+ P FD++ Q V +LFS+ L G +  
 Sbjct: 180 DGILGLAYPSIS--SSGATPVFDNIWNQGLVSQLDFSVYLSADD-----KSGSVV 227  
 Query: 136 IIGGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL 195  
 I GGID S YTGSL + P+ E Y+++ + +NG+ + C E ++IVD+GT+ L  
 Sbjct: 228 IFGGIDSSYYTGSLNWPVTVVEGYWQITVDSITMNETIA--CAE--GCQAIVDTGTSLL 283  
 Query: 196 RLPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLV-CWQAGTTPWNIFPVISLYLMGEVTN 254  
 P I A+ +++ G+ +V C + P +F T  
 Sbjct: 284 TGPTSPIANIQSDIGASENSD-----GDMVVSCSAISSLPDIVF-----TI 324  
 Query: 255 QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIG 314  
 + + P Y+ E S ++S ++G V + ++ VF+RA ++G  
 Sbjct: 325 NGVQYPVPPSAYILQSEGSCISGFQGMNVP-TESGELWILGDVFIRQYFTVFERANNQVG 383  
 Query: 315 FA 316  
 A  
 Sbjct: 384 LA 385

>SP:P14091|CATE\_HUMAN|CATHEPSIN E PRECURSOR (EC 3.4.23.34).  
 >PIR:A42038 A34401 S35663 S34467 A34643  
 B34643|A34401|cathepsin E (EC 3.4.23.34) precursor -  
 human >STR:CAB82850|CAB82850|Procathepsin E precursor  
 (EC 3.4.23.34). >GNP:AJ250717|AJ250717\_1|Homo sapiens  
 mRNA for procathepsin E (CatE gene).  
 >GNP:J05036|J05036\_1|Human cathepsin E mRNA, complete  
 cds; cathepsin E precursor. >GNP:M84424|M84424\_1|Human  
 cathepsin E (CTSE) gene, exon 9 and complete cds.  
 Length = 396

Score = 78.4 bits (190), Expect = 1e-14  
 Identities = 83/325 (25%), Positives = 137/325 (41%), Gaps = 46/325 (14%)

Query: 2 VPFIYL----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTV 56  
 VP +Y + H SSTY + + Y G G +G D VS+ G V  
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIQYGTGSLSGIIGADQVSV-EGLTVVG 162  
 Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDSPPEPFFDSLVLKQTHVPNLFSLQLC 116  
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +  
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ----NLVDLPMF 215  
 Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSPLYTGSWYTPIRREWYVEIIVRVEINGQDLKM 176  
 N G +I GG DHS ++GSL + P+ ++ Y+++ + +++ G M  
 Sbjct: 216 SVYMSSNPE--GGAGSELIFGGYDHSFSGSLNWPVTKQAYWQIALDNIQVGG--TVM 270  
 Query: 177 DCKEYNYDKSIVDSGTTNLRPLKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTT 236  
 C E ++IVD+GT+ + P + +I AA DG + E  
 Sbjct: 271 FCSE--GCQAIVDTGTSITGSPDKIKQLQNAIGAAP-----VDGEYAVE-----CA 315  
 Query: 237 PWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT- 292  
 N+ P ++ + G T+ P Y + D C ++ G  
 Sbjct: 316 NLNVMPDVTFTING-----VPYTLSPYAY--TLLDFVDGMQFCSSGFQGLDIHPAGPL 367  
 Query: 293 -VMGAVIMEGFYVVFDRARKRIGFA 316

++G V + FY VFDR R+G A  
 Sbjct: 368 WILGDVFIRQFYVSFDRGNRRVGLA 392

>SP:P07339|CATD\_HUMAN|CATHEPSIN D PRECURSOR (EC 3.4.23.5).  
 >GSP:R74207|R74207|Human death associated protein DAP-7,  
 also called cathepsin D. >GSP:W71369|W71369|Death  
 associated protein (DAP)-7 (cathepsin D).  
 >GSP:Y06478|Y06478|Human tumour-associated protein  
 PRO292. >PIR:A25771 S30749 PC2066 I59236  
 I57716|KHHUD|cathepsin D (EC 3.4.23.5) precursor  
 [validated] - human >GNP:X05344|X05344\_1|Human mRNA for  
 cathepsin D from oestrogen responsive breast cancer  
 cells; precursor polypeptide (AA -20 to 392).  
 >GNP:M63138|M63138\_1|Human cathepsin D (catD) gene,  
 exons 7, 8, and 9. >GNP:M11233|M11233\_1|Human cathepsin  
 D mRNA, complete cds; preprocathepsin D.  
 Length = 412

Score = 75.7 bits (183), Expect = 1e-13  
 Identities = 91/327 (27%), Positives = 138/327 (41%), Gaps = 53/327 (16%)

Query: 10 HFTLCSGWSSTYRDLRKGVVVPYTQGWEGELGTDLVSIHP-----GPNVTVRANI 60  
 H S SSTY + Y G G L D VS+P G R  
 Sbjct: 120 HHKYNDSKSSSTYVKNGTSTFDIHYGSGSLSGYLSQDTSVPCQSASSASALGGVKVERQVF 179  
 Query: 61 AAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSL VKQTHVP-NLFSLQLCGAG 119  
 T+ + ++GILG+AY I+ ++ P FD+L++Q V N+FS L  
 Sbjct: 180 GEATKQPGITFIAAKFDGILGMAYPRISV--NNVLPVFDNLMQQLVDQNIFS FYL---- 233  
 Query: 120 FPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEI-NGQDLKMD C 178  
 + A GG +++GG D Y GSL Y + R+ Y++V + +VE+ +G L C  
 Sbjct: 234 ----SRDPDAQPGGEIMLGGTDSKYKGSLSYLNVTRKAYWQVHLDQVEVASGLTL---C 286  
 Query: 179 KEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLV-CWQAGTTP 237  
 KE ++IVD+GT+ + P K+I A + GE ++ C + T  
 Sbjct: 287 KE--GCEAIVDTGTSLMVGPVDEVRELQKAIGAVPLIQ-----GEYMIPCEKVST-- 334  
 Query: 238 WNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQ-----SSTGT 292  
 P I+L L G+ S P+ Y V + C + S  
 Sbjct: 335 ---LPAILTKLGKGKYLKLS-----PEDYTLKVSQAGKTL--CLSGFMGMDIPPPSGPLW 383  
 Query: 293 VMGAVIMEGFYVVFDRARKRIGFAVSA 319  
 ++G V + +Y VFDR R+GFA +A  
 Sbjct: 384 ILGDVFIGRYTTFDRDNNRVGF AEAA 410

>SP:P20142|PEPC\_HUMAN|GASTRISIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN  
 C). >PIR:A29937 A31811 PX0028 I54213 A91125  
 A23458|A29937|gastricsin (EC 3.4.23.3) precursor - human  
 >GNP:U75272|U75272\_1|Human gastricsin mRNA, complete  
 cds; pepsinogen C; partial peptide sequencing.  
 >GNP:M23077|M23077\_1|Human pepsinogen gene, exon 9,  
 clone PCG401; precursor. >GNP:J04443|J04443\_1|Homo  
 sapiens pepsinogen C (PGC) mRNA, complete cds;  
 precursor.  
 Length = 388

Score = 71.4 bits (172), Expect = 2e-12  
 Identities = 78/329 (23%), Positives = 142/329 (42%), Gaps = 50/329 (15%)

Query: 2 VPFIYLQA-----HFTLCSGWSSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGPNVTV 56  
 VP +Y Q+ H SSTY + Y G G G D +++ ++ V  
 Sbjct: 99 VPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYSGSLTGFFGYDTLTVQ---SIQV 155  
 Query: 57 RANIAAITESDKFFINGSNW-----EGILGLAYAEIARPDSPPEFFDSL VKQTHVPN-L 110  
 ++E++ G+N+ +GI+GLAY ++ D +V++ + + +  
 Sbjct: 156 PNQEFGLSENEP----GTNFVYAQFDGIMGLAYPALSV--DEATTAMQGMVQEGALTSPV 209  
 Query: 111 FSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEIN 170  
 FS+ L S S GG+++ GG+D SLYTG +++ P+ +E Y+++ I I  
 Sbjct: 210 FSVYL-----SNQQGSSGGAUVFGGVDSLSYTGQIYWAPVTQELYWQIGIEEFLIG 260  
 Query: 171 GQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVC 230  
 GQ C E ++IVD+GT+ L +P++ A +++ A G+ LV  
 Sbjct: 261 GQASGW-CSE--GCQAIVDTGTSLLTVPQQYMSALLQATGAQEDE-----YGQFLV- 308

Query: 231 WQAGTTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSST 290  
 N + +L + + N + P Y+ T + +  
 Sbjct: 309 -----NCNSIQNLPSLTFTIIN-GVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQP 359

Query: 291 GTVMGAVIMEGFYVVFDRARKRIGFAVSA 319  
 ++G V + +Y V+D R+GFA +A  
 Sbjct: 360 LWILGDVFLRSYYSVYDLGNNRVGFATAA 388

>GNP:M18667|M18667\_1|Human pepsinogen C gene, exon 9, clone  
 cosHPGC44-1; prepropepsinogen C.  
 Length = 385

Score = 71.4 bits (172), Expect = 2e-12  
 Identities = 78/329 (23%), Positives = 142/329 (42%), Gaps = 50/329 (15%)

Query: 2 VPFIYLQA-----HFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56  
 VP +Y Q+ H SSTY + + Y G G G D +++ ++ V  
 Sbjct: 96 VPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYSGSLTGFFGYDTLTVQ---SIQV 152

Query: 57 RANIAAITESDKFFINGSNW-----EGILGLAYAEIARPDSPPEFFDSLQKTHVPN-L 110  
 ++E++ G+N+ +GI+GLAY ++ D +V++ + + +  
 Sbjct: 153 PNQEFGLSENEP----GTNFVYAQFDGIMGLAYPALSV--DEATTAMQGMVQEGALTSPV 206

Query: 111 FSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEVIIIVRVEIN 170  
 FS+ L S S GG+++ GG+D SLYTG +++ P+ +E Y+++ I I  
 Sbjct: 207 FSVYL-----SNQQGSSGGAUVFVGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIG 257

Query: 171 GQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVC 230  
 GQ C E ++IVD+GT+ L +P++ A +++ A G+ LV  
 Sbjct: 258 GQASGW-CSE--GCQAIVDTGTSLLTVPQQYMSALLQATGAQEDE-----YGQFLV- 305

Query: 231 WQAGTTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSST 290  
 N + +L + + N + P Y+ T + +  
 Sbjct: 306 -----NCNSIQNLPSLTFTIIN-GVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQP 356

Query: 291 GTVMGAVIMEGFYVVFDRARKRIGFAVSA 319  
 ++G V + +Y V+D R+GFA +A  
 Sbjct: 357 LWILGDVFLRSYYSVYDLGNNRVGFATAA 385

>GSP:Y31744|Y31744|Human protease HPRM-3.  
 Length = 349

Score = 62.8 bits (150), Expect = 7e-10  
 Identities = 47/168 (27%), Positives = 78/168 (45%), Gaps = 16/168 (9%)

Query: 2 VPFIYL-----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56  
 VP +Y + H SSTY + + Y G G +G D VS+ G V  
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIYGTGSLSGIIGADQVSV-EGLTVVG 162

Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLC 116  
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +  
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ---NLVDLPMF 215

Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEVII 164  
 N G +I GG DHS ++GSL + P+ ++ Y+++ +  
 Sbjct: 216 SVYMSSNPE--GGAGSELIFGGYDHSFSGSLNWVPVTKQAYWQIAL 260

>STR:CAB82849|CAB82849|Cathepsin E, alternative precursor (EC  
 3.4.23.34). >GNP:AJ250716|AJ250716\_1|Homo sapiens mRNA  
 for cathepsin E (CatE gene), alternative splicing,  
 isolated from adenocarcinoma cell lines.  
 Length = 363

Score = 62.8 bits (150), Expect = 7e-10  
 Identities = 47/168 (27%), Positives = 78/168 (45%), Gaps = 16/168 (9%)

Query: 2 VPFIYL-----QAHFTLCSGWSSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGPNVTV 56  
 VP +Y + H SSTY + + Y G G +G D VS+ G V  
 Sbjct: 104 VPSVYCTSPACKTHSRFQPSQSSTYSQPGQSFISIYGTGSLSGIIGADQVSV-EGLTVVG 162

Query: 57 RANIAAITESDKFFINGSNWEGILGLAYAEIARPDSPPEFFDSLQKTHVPNLFSLQLC 116  
 + ++TE + F++ + ++GILGL Y +A P FD+++ Q NL L +  
 Sbjct: 163 QQFGESVTEPGQTFVD-AEFDGILGLGYPSLAV--GGVTPVFDNMMAQ---NLVDLPMF 215

Query: 117 GAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVII 164  
                   N                  G +I GG DHS ++GSL + P+ ++ Y+++ +  
 Sbjct: 216 SVYMSSNPE---GGAGSELIFGGYDHSFSGSLNWVPVTKQAYWQIAL 260

>SP:P00797|RENI\_HUMAN|RENIN PRECURSOR, RENAL (EC 3.4.23.15)  
 (ANGIOTENSINOGENASE). >PIR:A21454 A21190 A21673 A00990  
 A26531 I52884 I55306 I53999 A35688 A36504 A27367  
 A39906|REHUK|renin (EC 3.4.23.15) precursor - human  
 >GNP:L00073|L00073\_1|Human renin gene, exon 10;  
 precursor. >GNP:M10152|M10152\_1|Human renin gene, exon  
 10.  
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07  
 Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

Query: 18 SSTRDLRKGYYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
           SS+Y+       + + Y+ G   G L D++++       +TV       +TE       + ++  
 Sbjct: 135 SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78 GILGLAYAEIARDDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136  
           G++G+ + E A       P FD+++ Q + ++FS       +   SE   S+GG ++  
 Sbjct: 192 GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 243

Query: 137 IGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196  
           +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +  
 Sbjct: 244 LGGSDPQHYEGNFHYINLIKTGVWQIQMKGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256  
                           + SS EK +       ++L +       P IS +L G+  
 Sbjct: 300 -----GSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311  
           T+   Y+   ++ +S+ C   +   I + T +GA + FY FDR  
 Sbjct: 342 -EYTLTSADYV--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312 RIGFAVS 318  
           RIGFA++  
 Sbjct: 399 RIGFALA 405

>GSP:P50135|P50135|Sequence of pre-pro-renin.  
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07  
 Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

Query: 18 SSTRDLRKGYYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
           SS+Y+       + + Y+ G   G L D++++       +TV       +TE       + ++  
 Sbjct: 135 SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78 GILGLAYAEIARDDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136  
           G++G+ + E A       P FD+++ Q + ++FS       +   SE   S+GG ++  
 Sbjct: 192 GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 243

Query: 137 IGGIDHSLYTGSLWYTPIRREWYEVIIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196  
           +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +  
 Sbjct: 244 LGGSDPQHYEGNFHYINLIKTGVWQIQMKGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256  
                           + SS EK +       ++L +       P IS +L G+  
 Sbjct: 300 -----GSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311  
           T+   Y+   ++ +S+ C   +   I + T +GA + FY FDR  
 Sbjct: 342 -EYTLTSADYV--FQESYSSKKLCTLAHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312 RIGFAVS 318  
           RIGFA++  
 Sbjct: 399 RIGFALA 405

>GSP:W23244|W23244|Human renin.  
 Length = 406

Score = 55.4 bits (131), Expect = 1e-07

Identities = 66/307 (21%), Positives = 129/307 (41%), Gaps = 42/307 (13%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 135  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 191

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      + SE S+GG ++
Sbjct: 192  GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 243

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 244  LGGSDPQHIEGNFHYINLIKTVGWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 299

Query: 197  LPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256
          + SS EK +   ++L +   P IS +L G+
Sbjct: 300  -----GSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGK----- 341

Query: 257  FRITILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
          T+   Y+   ++ +S+ C   + I + T +GA + FY FDR
Sbjct: 342  -EYTLTSADYV--FQESYSSKKLCTLAIHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 398

Query: 312  RIGFAVS 318
          RIGFA++
Sbjct: 399  RIGFALA 405

```

>STR:Q15296|Q15296|KIDNEY MRNA FRAGMENT FOR RENIN (AA 105-401)  
 (FRAGMENT). >GNP:X00063|X00063\_1|Human kidney mRNA  
 fragment for renin (aa 105-401); renin (aa 105 to 401).  
 Length = 300

Score = 55.0 bits (130), Expect = 2e-07

Identities = 70/307 (22%), Positives = 133/307 (42%), Gaps = 41/307 (13%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 28  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAEFD 84

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      + SE S+GG ++
Sbjct: 85  GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFSF-----YYNRDSENSQSLGGQIV 136

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 137  LGGSDPQHIEGNFHYINLIKTVGWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 192

Query: 197  LPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256
          E   K ++A + EK      L + +V   G T   P IS +L G+
Sbjct: 193  GSTSSIE---KLMEALGAKEKR-----LFDYVVKCNEGPT----LPDISFHLGGK----- 235

Query: 257  FRITILPQQYLRPVEDVATSQDDC---YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311
          T+   Y+   ++ +S+ C   + I + T +GA + FY FDR
Sbjct: 236  -EYTLTSADYI--FQESYSSKKLCTLAIHAMDIPPTGPTWALGATFIRKFYTEFDRRNN 292

Query: 312  RIGFAVS 318
          RIGFA++
Sbjct: 293  RIGFALA 299

```

>GNP:M26901|M26901\_1|Human renin gene, exon 9; precursor.  
 Length = 403

Score = 52.3 bits (123), Expect = 1e-06

Identities = 67/307 (21%), Positives = 132/307 (42%), Gaps = 45/307 (14%)

```

Query: 18  SSTYRDLRKGVPYPTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77
          SS+Y+      + + Y+ G   G L D++++      +TV      +TE      + ++
Sbjct: 135  SSSYKHNGTELTLRYSTGTVSGFLSQDIITVG---GITVTQMFGEVTEMPALPFMLAQFD 191

Query: 78  GILGLAYAEIARPDSPPEFFDSLQKTHVP-NLFSLQLCGAGFPLNQSEVLASVGGSMI 136
          G++G+ + E A      P FD+++ Q + ++FS      F N++ S+GG ++
Sbjct: 192  GVVGMGFIEQAI--GRVTPIFDNIISQGVLKEDVFS-----FYYNRNS--QSLGGQIV 240

Query: 137  IGGIDHSLYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196
          +GG D   Y G+   Y + +   +++ + V +   L +   +   ++VD+G + +
Sbjct: 241  LGGSDPQHIEGNFHYINLIKTVGWQIQMGVSVGSSTLLCE----DGCLALVDTGASYIS 296

```



Query: 197 LPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQS 256  
 E ++++ A L + +V G T P IS +L G+  
 Sbjct: 297 GSTSCIEKLMEALGAKKR-----LFDYVVVKNEGPT----LPDISFHLGGK----- 338

Query: 257 FRITILPQQYLRPVEDVATSQDDC----YKFAISQSSTGT-VMGAVIMEGFYVVFDRARK 311  
 T+ Y+ ++ +S+ C + I + T +GA + FY FDR  
 Sbjct: 339 -EYTLTSADYV--FQESYSSKKLCTLAIHAMDIPPTGPTWALGATFIRKFYTEFDRRN 395

Query: 312 RIGFAVS 318  
 RIGFA++  
 Sbjct: 396 RIGFALA 402

>GSP:W54877|W54877|Human napsin A protein.  
 Length = 451

Score = 37.5 bits (85), Expect = 0.030  
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
 SS+++ + Y G+ +G L D ++I +V A S F + S +  
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136  
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++  
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172  
 +GG D + Y L + P+ Y+++ + RV++ +  
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>GSP:W57042|W57042|Human aspartic protease SEQ ID NO:1.  
 Length = 438

Score = 37.5 bits (85), Expect = 0.030  
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
 SS+++ + Y G+ +G L D ++I +V A S F + S +  
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136  
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++  
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172  
 +GG D + Y L + P+ Y+++ + RV++ +  
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>GSP:Y44810|Y44810|Human Aspartic Protease-2 (NHAP-2).  
 Length = 433

Score = 37.5 bits (85), Expect = 0.030  
 Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVVVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
 SS+++ + Y G+ +G L D ++I +V A S F + S +  
 Sbjct: 127 SSSFKPSGKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136  
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++  
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQ 172  
 +GG D + Y L + P+ Y+++ + RV++ +  
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>STR:Q9UHB3|Q9UHB3|ASPARTYL PROTEASE 3 (FRAGMENT).  
 >GNP:AF200344|AF200344\_1|Homo sapiens aspartyl protease  
 3 mRNA, partial cds.  
 Length = 450

Score = 37.5 bits (85), Expect = 0.030

Identities = 39/156 (25%), Positives = 72/156 (46%), Gaps = 13/156 (8%)

Query: 18 SSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
 SS+++ + Y G+ +G L D ++I +V A S F + S +  
 Sbjct: 127 SSSFKPSGKTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 184

Query: 78 GILGLAYAEIARPDDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136  
 GILGL + ++ + P D LV+Q + +FS F N+ +A GG ++  
 Sbjct: 185 GILGLGFPILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRDPEVAD-GGELV 234

Query: 137 IGGIDHSLYTGS LWYTPIRREWYVEIIVRVEINGQ 172  
 +GG D + Y L + P+ Y+++ + RV++ +  
 Sbjct: 235 LGGSDPAHYIPPLTFVPVTVPAYWQIHMERVKVGSR 270

>SP:096009|NAP1\_HUMAN|NAPSIN 1 PRECURSOR (EC 3.4.23.-) (NAPSIN A)  
 (NAP1) (TA01/TA02) (ASPARTYL PROTEASE 4) (ASP 4) (ASP4).  
 >GSP:W54878|W54878|Human napsin B protein.  
 >GNP:AF090386|AF090386\_1|Homo sapiens napsin A mRNA,  
 complete cds; aspartic proteinase.  
 >GNP:AF098484|AF098484\_1|Homo sapiens napsin 1  
 precursor, mRNA, complete cds.  
 >GNP:AF200345|AF200345\_1|Homo sapiens aspartyl protease  
 4 mRNA, complete cds.  
 Length = 420

Score = 36.7 bits (83), Expect = 0.052  
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE GILGLAYAEIAR 89  
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++  
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148  
 + P D LV+Q + +FS F LN+ GG +++GG D + Y  
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKKVFEA 204  
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A  
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAKGC---AAILDTGTSLITGPTEEIRA 298

>GSP:W37958|W37958|Amino acid sequence of human cathepsin  
 polypeptide-2.  
 Length = 395

Score = 36.7 bits (83), Expect = 0.052  
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE GILGLAYAEIAR 89  
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++  
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148  
 + P D LV+Q + +FS F LN+ GG +++GG D + Y  
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKKVFEA 204  
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A  
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAKGC---AAILDTGTSLITGPTEEIRA 298

>GSP:Y06435|Y06435|Human protease HUPM-4. >GSP:Y44809|Y44809|Human  
 Aspartic Protease-1 (NHAP-1). >GSP:Y44457|Y44457|Human  
 lung specific gene protein Lngl05.  
 Length = 420

Score = 36.7 bits (83), Expect = 0.052  
 Identities = 45/176 (25%), Positives = 82/176 (46%), Gaps = 17/176 (9%)

Query: 30 VPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE GILGLAYAEIAR 89  
 + Y G+ +G L D ++I +V A S F ++++GILGL + ++  
 Sbjct: 139 IQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWEP SLVFAF--AHFDGILGLGFPILSV 196

Query: 90 PDDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI IGGIDHSLYTGS 148  
 + P D LV+Q + +FS F LN+ GG +++GG D + Y  
 Sbjct: 197 --EGVRPPMDVLVEQGLLDKPVFS-----FYLNRDPEEPD-GGELVLGGSDPAHYIPP 246

Query: 149 LWYTPIRREWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204  
 L + P+ Y+++ + RV++ G L + K +I+D+GT+ + P + A  
 Sbjct: 247 LTFVPVTVPAYWQIHMERVKV-GPGLTLCAGKC---AAILDTGTSITGPTTEEIRA 298

>GSP:W57043|W57043|Human aspartic protease encoding cDNA SEQ ID  
 NO:15.  
 Length = 449

Score = 36.0 bits (81), Expect = 0.088  
 Identities = 44/178 (24%), Positives = 80/178 (44%), Gaps = 21/178 (11%)

Query: 18 SSTYRDLRKGVVYPYTQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWE 77  
 SS+++ + Y G+ +G L D ++I +V A S F + S +  
 Sbjct: 146 SSSFKPSGKTKFAIQYGTGRVDGILSEDKLTIGGIKGASVIFGEALWESSLVFTV--SRPD 203

Query: 78 GILGLAYAEIARPDSPPEFFDSLQKTHVPN-LFSLQLCGAGFPLNQSEVLASVGGSMI 136  
 GILGL + ++ + P D LV+Q + +FS F N+ + + GG ++  
 Sbjct: 204 GILGLGFILSV--EGVRPPLDVLVEQGLLDKPVFS-----FYFNRPDPEVVN-GGELV 253

Query: 137 IGGIDHSLYTGSWYTPIRREWYVEIIVRVEI--NGQDLKMDCKEYNYDKSIVDSGT 192  
 +GG D + Y L + P+ Y+++ + RV++ L C +I+D+GT  
 Sbjct: 254 LGGSDPAHYIPPLNFVPVTVPAYWQIHMERVKVGPRA DSLCQGC-----AAILDTGT 305

>PIR:T08737|T08737|hypothetical protein DKFZp566O1646.1 - human  
 (fragment) >STR:Q9Y415|Q9Y415|HYPOTHETICAL 25.3 KDA  
 PROTEIN (FRAGMENT). >GNP:AL050084|AL050084\_1|Homo  
 sapiens mRNA; cDNA DKFZp566O1646 (from clone  
 DKFZp566O1646); partial cds; weak similarity to  
 S.cerevisiae Zip1p.  
 Length = 218

Score = 33.6 bits (75), Expect = 0.45  
 Identities = 20/67 (29%), Positives = 32/67 (46%), Gaps = 12/67 (17%)

Query: 157 EWYVEIIVR-VEINGQ-----DLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204  
 +W +E + + INGQ D + E +D+ IVD T + P+K+ E  
 Sbjct: 14 QWTFESAVQENISINGQAWQEASDNCFMDSIKVLEDQFDEIIVDIATKRKQYPRKILEC 73

Query: 205 AVKSIKA 211  
 +K+IKA  
 Sbjct: 74 VIKTIKA 80

>STR:AAF86877|AAF86877|DC8. >GNP:AF201941|AF201941\_1|Homo sapiens  
 DC8 (DC8) mRNA, complete cds.  
 Length = 268

Score = 33.6 bits (75), Expect = 0.45  
 Identities = 20/67 (29%), Positives = 32/67 (46%), Gaps = 12/67 (17%)

Query: 157 EWYVEIIVR-VEINGQ-----DLKMDCKEYNYDKSIVDSGTTNLRPKKVFEA 204  
 +W +E + + INGQ D + E +D+ IVD T + P+K+ E  
 Sbjct: 64 QWTFESAVQENISINGQAWQEASDNCFMDSIKVLEDQFDEIIVDIATKRKQYPRKILEC 123

Query: 205 AVKSIKA 211  
 +K+IKA  
 Sbjct: 124 VIKTIKA 130

>RTR:AAD53859|AAD53859|IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
 (FRAGMENT). >GNP:AF174113|AF174113\_1|Homo sapiens clone  
 sc77u-36 immunoglobulin heavy chain variable region  
 (IgH) mRNA, partial cds.  
 Length = 122

Score = 31.7 bits (70), Expect = 1.7  
 Identities = 27/101 (26%), Positives = 44/101 (42%), Gaps = 21/101 (20%)

Query: 143 SLYTGSLSWYTPIRR-----EWYVEIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR 196  
 S+ +GS +++ IR+ EW I R+ +G NY+ S+ T ++  
 Sbjct: 28 SISSGSYYWSWIRQPAGKGLEW-----IGRIYTSGST-----NYNPSLKSRTVISVD 74

Query: 197 LPKKVFEAAVKSIIKAASSTEKF--PDGFWLGEQLVCWQAGT 235  
 K F + S+ AA + + DG W GE + W GT

Sbjct: 75 TSKNQFSLKLSSVTAADTAVYYCARDGLWFGFISHWGQGT 115

>SP:Q99712 Q99446 O00564|IRKF\_HUMAN|ATP-SENSITIVE INWARD RECTIFIER  
 POTASSIUM CHANNEL 15 (POTASSIUMCHANNEL, INWARDLY  
 RECTIFYING, SUBFAMILY J, MEMBER 15) (INWARDRECTIFIER  
 POTASSIUM CHANNEL KIR 4.2) (KIR1.3).  
 >GSP:W26369|W26369|Human kidney inward rectifier K  
 channel 3 (KIRK-3). >GNP:U73191|U73191\_1|Human inward  
 rectifier potassium channel (Kir1.3), complete cds.  
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSlyTGSLWYTPIRREWYEVII 164  
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +  
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

>GNP:D87291|D87291\_1|Human mRNA for inward rectifier potassium  
 channel, complete cds; human homolog of rat inward  
 rectifier potassium channel 10.  
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSlyTGSLWYTPIRREWYEVII 164  
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +  
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

>GNP:Y10745|Y10745\_1|H.sapiens mRNA for inwardly rectifying potassium  
 channel Kir4.2.  
 Length = 375

Score = 29.3 bits (64), Expect = 8.7

Identities = 17/52 (32%), Positives = 27/52 (51%), Gaps = 5/52 (9%)

Query: 117 GAGFPLNQSEVLASVGGSMI----IGGIDHSlyTGSLWYTPIRREWYEVII 164  
 GAG N+ V++ G S + + GI + LY LW T I +W Y++ +  
 Sbjct: 19 GAGLKANRPRVMSKSGHSNVRIDKVDGI-YLLYLQDLWTTVIDMKWRYKLTL 69

Database: /nfs/banks2/index/data/blast/smartSorted/PROT/homosapiens

Posted date: Oct 5, 2000 10:09 AM

Number of letters in database: 24,820,038

Number of sequences in database: 113,759

Lambda	K	H
0.321	0.138	0.435

Gapped		
Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 18424685

Number of Sequences: 113759

Number of extensions: 771118

Number of successful extensions: 1268

Number of sequences better than 10.0: 50

Number of HSP's better than 10.0 without gapping: 45

Number of HSP's successfully gapped in prelim test: 5

Number of HSP's that attempted gapping in prelim test: 1184

Number of HSP's gapped (non-prelim): 60

length of query: 351

length of database: 24,820,038

effective HSP length: 47

effective length of query: 304

effective length of database: 19473365

effective search space: 5919902960

effective search space used: 5919902960

T: 11